



IFWO

## RAW SEQUENCE LISTING

DATE: 09/08/2004

PATENT APPLICATION: US/10/767,325

TIME: 11:57:00

Input Set : A:\08737-1.txt

Output Set: N:\CRF4\09082004\J767325.raw

3 <110> APPLICANT: Ross, Theodora  
 4 Mizukami, Ikuko  
 6 <120> TITLE OF INVENTION: Humoral Response to H1P1 in Cancer  
 8 <130> FILE REFERENCE: UM-08737  
 10 <140> CURRENT APPLICATION NUMBER: 10/767,325  
 11 <141> CURRENT FILING DATE: 2004-01-29  
 13 <160> NUMBER OF SEQ ID NOS: 6  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 4534  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: misc\_feature  
 25 <222> LOCATION: (4521)..(4522)  
 26 <223> OTHER INFORMATION: n is a, c, g, or t  
 28 <400> SEQUENCE: 1



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31	gatcggaatg	ccagctccat	gaagcagggt	cccaaccac	tgccaaggt	gctgagccgg	120
33	cgcgggggtc	gcgctgggct	ggaggcggcg	gagcgcgaga	gcttcgagcg	gactcagact	180
35	gtcagcatca	ataaggccat	taatacgcat	gaagtggctg	taaaggaaaa	acacgccaga	240
37	acgtgcatac	tgggcaccca	ccatgagaaa	ggggcacaga	ccttctggtc	tggtgtcaac	300
39	cgcctgcctc	tgtctagcaa	cgcagtgtct	tgttggaagt	tctgccatgt	gttccacaaa	360
41	ctcctccgag	atggacaccc	gaacgtcctg	aaggactctc	tgagatacag	aatgaattg	420
43	agtgcacatg	gcaggtatgt	gggtacactg	agcgagggtg	atggccagct	gtgcagcatc	480
45	tacctgaaac	tgctaagaac	caagatggag	taccacacca	aaaatcccag	gttcccaggc	540
47	aacctgcaga	tgagtgaccg	ccagctggac	gaggctggag	aaagtgcagt	gaacaacttt	600
49	tcccagttaa	cagtggagat	gtttgactac	ctggagtgtg	aactcaacct	cttccaaaca	660
51	gtattcaact	ccctggacat	gtcccgtctt	gtgtccgtga	cggcagcagg	gcagtgcgcg	720
53	ctcgcgccgc	tgatccaggt	catcttgac	tgcagccacc	tttatgacta	caactgtcaag	780
55	cttctcttca	aactccactc	ctgcctccca	gctgacaccc	tgcaaggcca	ccgggaccgc	840
57	ttcatggagc	agtttacaaa	gttgaaagat	ctgttctacc	gctccagcaa	cctgcagtac	900
59	ttcaagcggc	tcattcagat	ccccagctg	cctgagaacc	caaccaactt	cctgcgagcc	960
61	tcagccctgt	cagaacatat	cagccctgtg	gtggtgatcc	ctgcagaggc	ctcatcccc	1020
63	gacagcgagc	cagtcctaga	gaaggatgac	ctcatggaca	tggatgcctc	tcagcagaat	1080
65	ttatttgaca	acaagtttga	tgacatcttt	ggcagttcat	tcagcagtga	tccttcaat	1140
67	ttcaacagtc	aaaatggtgt	gaacaaggat	gagaaggacc	acttaattga	gcgactatac	1200
69	agagagatca	gtggattgaa	ggcacagcta	gaaaacatga	agactgagag	ccagcgggtt	1260
71	gtgctgcagc	tgaagggccg	cgtcagcgag	ctggaagcag	atctggccga	gcagcagcac	1320
73	ctgcggcagc	aggcggccga	cgactgtgaa	ttcctgcggg	cagaactgga	cgagctcagg	1380
75	aggcagcggg	aggacaccga	gaaggctcag	cggagcctgt	ctgagataga	aaggaaagct	1440
77	caagccaatg	aacagcgata	tagcaagcta	aaggagaagt	acagcgagct	ggttcagaac	1500
79	cacgctgacc	tgctgcggaa	gaatgcagag	gtgaccaaac	aggtgtccat	ggccagacaa	1560

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85	cttgccacaa	gccaacggga	gcttcagggt	ctgcaaggca	gcctggaaac	ttctgcccag	1740
87	tcagaagcaa	actgggcagc	cgagttcgcc	gagctagaga	aggagcggga	cagcctggtg	1800
89	agtggcgag	ctcataggga	ggaggaatta	tctgctcttc	ggaaagaact	gcaggacact	1860
91	cagctcaaac	tggccagcac	agaggaatct	atgtgccagc	ttgccaaaga	ccaacgaaaa	1920
93	atgcttctgg	tggggtccag	gaaggctgcg	gagcaggtga	tacaagacgc	cctgaaccag	1980
95	cttgaagaac	ctcctctcat	cagctgcgct	gggtctgcag	atcacctcct	ctccacggtc	2040
97	acatccattt	ccagctgcat	cgagcaactg	gagaaaagct	ggagccagta	tctggcctgc	2100
99	ccagaagaca	tcagtggact	tctccattcc	ataaccctgc	tggcccactt	gaccagcgac	2160
101	gccattgctc	atgggtgccac	cacctgcctc	agagccccac	ctgagcctgc	cgactcactg	2220
103	accgaggcct	gtaagcagta	tggcagggaa	accctcgctc	acctggcctc	cctggaggaa	2280
105	gaggaagcc	ttgagaatgc	cgacagcaca	gccatgagga	actgcctgag	caagatcaag	2340
107	gcatcggcg	aggagctcct	gcccagggga	ctggacatca	agcaggaggga	gctggggggac	2400
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111	gaggagatgc	tcagcaaate	ccgagcagga	gacacaggag	tcaaatggga	ggtgaatgaa	2520
113	aggatccttg	gttgcctgtac	cagcctcatg	caagctattc	aggtgctcat	cgtggcctct	2580
115	aaggacctcc	agagagagat	tgtggagagc	ggcaggggta	cagcatcccc	taaagagttt	2640
117	tatgccaaaga	actctcgatg	gacagaagga	cttatctcag	cctccaaggc	tgtgggctgg	2700
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121	gagctaattg	tgtgtttctca	tgaaattgct	gctagcacag	cccagcttgt	ggctgcatcc	2820
123	aagtgaaag	ctgataagga	cagccccaac	ctagcccagc	tgcagcaggc	ctctcgggga	2880
125	gtgaaccagg	ccactgccgg	cgttgtggcc	tcaaccattt	ccggcaaate	acagatcgaa	2940
127	gagacagaca	acatggactt	ctcaagcatg	acgctgacac	agatcaaacg	ccaagagatg	3000
129	gattctcagg	ttaggggtgct	agagctagaa	aatgaattgc	agaaggagcg	tcaaaaactg	3060
131	ggagagcttc	ggaaaaagca	ctacgagctt	gctggtgttg	ctgagggctg	ggaagaagga	3120
133	acagaggcat	ctccacctac	actgcaagaa	gtggttaaccg	aaaaagaata	gagccaaacc	3180
135	aacacccccat	atgtcagtg	aaatccttgt	tacatatctc	gtgtgtgtta	tttccccagc	3240
137	cacaggccaa	atccttggag	tcccaggggc	agccacacca	ctgccattac	ccagtgcgga	3300
139	ggacatgcac	gacacttcca	aagactccct	ccatagcgac	accctttctg	tttggaccca	3360
141	tggatttcca	ctgcttctta	tgggtggttg	ttgggttttt	tgggtttgtt	tttttttttt	3420
143	aagtttccact	cacatagcca	actctcccaa	agggcacacc	cctggggctg	agtctccagg	3480
145	gccccccaac	tgtggtagct	ccagcgatgg	tgtgcccag	gcctctcggt	gctccatctc	3540
147	cgctccaca	ctgaccaagt	gctggcccac	ccagtccatg	ctccagggtc	aggcggagct	3600
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151	tgaatcccg	cggaaagcct	ctgtccgcct	ttacaaggga	gaagacaaca	gaaagaggga	3720
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155	aatggagctg	gtgagatcaa	caacactact	tccctgccgg	aatgaactgt	ccgtgaatgg	3840
157	tctctgtcaa	gcgggcccgc	tcccttggcc	cagagacgga	gtgtgggagt	gattcccaac	3900
159	tcctttctgc	agacgtctgc	cttggcatcc	tcttgaatag	gaagatcggt	ccaccttcta	3960
161	cgcaattgac	aaacccggaa	gatcagatgc	aattgctccc	atcagggag	aaccctatac	4020
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165	agatgcttgg	agcaatcaga	acttcagggtg	tgactctagc	aaagctcatc	tttctgcccg	4140
167	gctacatcag	ccttcaagaa	tcagaagaaa	ggccaagggtg	ctggactggt	actgacttgg	4200
169	atcccaaagc	aaggagatca	tttggagctc	ttgggtcaga	gaaaatgaga	aaggacagag	4260
171	ccagcggctc	caactccttt	cagccacatg	ccccaggtc	tcgctgccc	gtggacagga	4320
173	tggagacaga	gggacacatg	acagcttgcc	agggatgggc	agcccaacag	cacttttctt	4380
175	cttctagatg	gaccccagca	tttaagtgc	cttctgatct	tgggaaaaca	gcgtcttctt	4440
177	tctttatcta	tagcaactca	ttggtggtag	ccatcaagca	cttcggaatt	cctgcagccc	4500

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W--> 179 gggcgggccgc tcgagcatgc nntagagggc ccta 4534

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183 <211> LENGTH: 1475

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190 <222> LOCATION: (1037)..(1038)

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193 <221> NAME/KEY: NON\_CONS

194 <222> LOCATION: (1083)..(1084)

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197 <221> NAME/KEY: NON\_CONS

198 <222> LOCATION: (1090)..(1091)

200 <220> FEATURE:

201 <221> NAME/KEY: NON\_CONS

202 <222> LOCATION: (1134)..(1135)

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205 <221> NAME/KEY: NON\_CONS

206 <222> LOCATION: (1142)..(1143)

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209 <221> NAME/KEY: NON\_CONS

210 <222> LOCATION: (1178)..(1179)

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213 <221> NAME/KEY: NON\_CONS

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217 <221> NAME/KEY: NON\_CONS

218 <222> LOCATION: (1194)..(1195)

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222 <222> LOCATION: (1247)..(1248)

224 <220> FEATURE:

225 <221> NAME/KEY: NON\_CONS

226 <222> LOCATION: (1283)..(1284)

228 <220> FEATURE:

229 <221> NAME/KEY: NON\_CONS

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232 <220> FEATURE:

233 <221> NAME/KEY: NON\_CONS

234 <222> LOCATION: (1315)..(1316)

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237 <221> NAME/KEY: NON\_CONS

238 <222> LOCATION: (1339)..(1340)

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Input Set : A:\08737~1.txt

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246 <222> LOCATION: (1382)..(1383)  
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 253 <221> NAME/KEY: NON\_CONS  
 254 <222> LOCATION: (1454)..(1455)  
 256 <220> FEATURE:  
 257 <221> NAME/KEY: misc\_feature  
 258 <222> LOCATION: (1472)..(1472)  
 259 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
 261 <400> SEQUENCE: 2  
 263 Met Asp Arg Met Ala Ser Ser Met Lys Gln Val Pro Asn Pro Leu Pro  
 264 1 5 10 15  
 267 Lys Val Leu Ser Arg Arg Gly Val Gly Ala Gly Leu Glu Ala Ala Glu  
 268 20 25 30  
 271 Arg Glu Ser Phe Glu Arg Thr Gln Thr Val Ser Ile Asn Lys Ala Ile  
 272 35 40 45  
 275 Asn Thr Gln Glu Val Ala Val Lys Glu Lys His Ala Arg Thr Cys Ile  
 276 50 55 60  
 279 Leu Gly Thr His His Glu Lys Gly Ala Gln Thr Phe Trp Ser Val Val  
 280 65 70 75 80  
 283 Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu Cys Trp Lys Phe Cys  
 284 85 90 95  
 287 His Val Phe His Lys Leu Leu Arg Asp Gly His Pro Asn Val Leu Lys  
 288 100 105 110  
 291 Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp Met Ser Arg Met Trp  
 292 115 120 125  
 295 Gly Tyr Leu Ser Glu Gly Tyr Gly Gln Leu Cys Ser Ile Tyr Leu Lys  
 296 130 135 140  
 299 Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys Asn Pro Arg Phe Pro  
 300 145 150 155 160  
 303 Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp Glu Ala Gly Glu Ser  
 304 165 170 175  
 307 Asp Val Asn Asn Phe Ser Gln Leu Thr Val Glu Met Phe Asp Tyr Leu  
 308 180 185 190  
 311 Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe Asn Ser Leu Asp Met  
 312 195 200 205  
 315 Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln Cys Arg Leu Ala Pro  
 316 210 215 220  
 319 Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu Tyr Asp Tyr Thr Val  
 320 225 230 235 240  
 323 Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro Ala Asp Thr Leu Gln  
 324 245 250 255  
 327 Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr Lys Leu Lys Asp Leu  
 328 260 265 270  
 331 Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys Arg Leu Ile Gln Ile  
 332 275 280 285  
 335 Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu Arg Ala Ser Ala Leu

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340 305      310      315      320
343 Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp Leu Met Asp Met Asp
344      325      330      335
347 Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe Asp Asp Ile Phe Gly
348      340      345      350
351 Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn Ser Gln Asn Gly Val
352      355      360      365
355 Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg Leu Tyr Arg Glu Ile
356      370      375      380
359 Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys Thr Glu Ser Gln Arg
360 385      390      395      400
363 Val Val Leu Gln Leu Lys Gly His Val Ser Glu Leu Glu Ala Asp Leu
364      405      410      415
367 Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala Asp Asp Cys Glu Phe
368      420      425      430
371 Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln Arg Glu Asp Thr Glu
372      435      440      445
375 Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys Ala Gln Ala Asn
376      450      455      460
379 Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser Glu Leu Val Gln
380 465      470      475      480
383 Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val Thr Lys Gln Val
384      485      490      495
387 Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg Glu Lys Lys Glu
388      500      505      510
391 Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly Gln Arg Lys Thr
392      515      520      525
395 Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln Glu Leu Ala Thr
396      530      535      540
399 Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu Glu Thr Ser Ala
400 545      550      555      560
403 Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu Leu Glu Lys Glu
404      565      570      575
407 Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu Glu Glu Leu Ser
408      580      585      590
411 Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys Leu Ala Ser Thr
412      595      600      605
415 Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg Lys Met Leu Leu
416      610      615      620
419 Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile Gln Asp Ala Leu Asn
420 625      630      635      640
423 Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala Gly Ser Ala Asp His
424      645      650      655
427 Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys Ile Glu Gln Leu Glu
428      660      665      670
431 Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu Asp Ile Ser Gly Leu
432      675      680      685

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 4521, 4522

Seq#:2; Xaa Pos. 1472 ✓

**VERIFICATION SUMMARY**

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Input Set : A:\08737~1.txt

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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:4500

L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1458